



#16
cont

SEQUENCE LISTING

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SNEDDEN, Wayne
AHARON, Gilad

<120> GENETIC ENGINEERING SALT TOLERANCE IN CROP PLANTS

<140> US 09/271,584

<141> 1999-03-18

<150> PCT/CA99/00219

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<150> US 60/078,474

<151> 1998-04-01

<150> US 60/116,111

<151> 1999-01-15

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<170> PatentIn Ver. 2.1, Word 97

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<222> (286)..(1899)

<223> Figure 1(a)

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Met Leu Asp Ser
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cta gtg tcg aaa ctg cct tcg tta tcg aca tct gat cac gct tct gtg 345
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gtt gcg ttg aat ctc ttt gtt gca ctt ctt tgt gct tgt att gtt ctt 393
Val Ala Leu Asn Leu Phe Val Ala Leu Leu Cys Ala Cys Ile Val Leu
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Gly His Leu Leu Glu Glu Asn Arg Trp Met Asn Glu Ser Ile Thr Ala	
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ttg ttg att ggg cta ggc act ggt gtt acc att ttg ttg att agt aaa	489
Leu Leu Ile Gly Leu Gly Thr Gly Val Thr Ile Leu Leu Ile Ser Lys	
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Gly Lys Ser Ser His Leu Leu Val Phe Ser Glu Asp Leu Phe Phe Ile	
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Lys Gln Phe Phe Arg Asn Phe Val Thr Ile Met Leu Phe Gly Ala Val	
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ggg act att att tct tgc aca atc ata tct cta ggt gta aca cag ttc	681
Gly Thr Ile Ile Ser Cys Thr Ile Ile Ser Leu Gly Val Thr Gln Phe	
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ttt aag aag ttg gac att gga acc ttt gac ttg ggt gat tat ctt gct	729
Phe Lys Lys Leu Asp Ile Gly Thr Phe Asp Leu Gly Asp Tyr Leu Ala	
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Ile Gly Ala Ile Phe Ala Ala Thr Asp Ser Val Cys Thr Leu Gln Val	
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ctg aat caa gac gag aca cct ttg ctt tac agt ctt gta ttc gga gag	825
Leu Asn Gln Asp Glu Thr Pro Leu Leu Tyr Ser Leu Val Phe Gly Glu	
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Gly Val Val Asn Asp Ala Thr Ser Val Val Val Phe Asn Ala Ile Gln	
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Ser Phe Asp Leu Thr His Leu Asn His Glu Ala Ala Phe His Leu Leu	
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Gly Asn Phe Leu Tyr Leu Phe Leu Leu Ser Thr Leu Leu Gly Ala Ala	
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acc ggt ctg ata agt gcg tat gtt atc aag aag cta tac ttt gga agg	1017
Thr Gly Leu Ile Ser Ala Tyr Val Ile Lys Lys Leu Tyr Phe Gly Arg	
230 235 240	
cac tca act gac cga gag gtt gcc ctt atg atg ctt atg gcg tat ctt	1065
His Ser Thr Asp Arg Glu Val Ala Leu Met Met Leu Met Ala Tyr Leu	
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tct tat atg ctt gct gag ctt ttc gac ttg agc ggt atc ctc act gtg	1113
Ser Tyr Met Leu Ala Glu Leu Phe Asp Leu Ser Gly Ile Leu Thr Val	
265 270 275	
ttt ttc tgt ggt att gtg atg tcc cat tac aca tgg cac aat gta acg	1161
Phe Phe Cys Gly Ile Val Met Ser His Tyr Thr Trp His Asn Val Thr	
280 285 290	
gag agc tca aga ata aca aca aag cat acc ttt gca act ttg tca ttt	1209
Glu Ser Ser Arg Ile Thr Thr Lys His Thr Phe Ala Thr Leu Ser Phe	
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Ile Asp Lys Trp Arg Ser Val Ser Asp Thr Pro Gly Thr Ser Ile Ala	
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ata act gtc tgt ctt ttt agc aca gtg gtg ttt ggt atg ctg acc aaa	1593
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425 430 435	
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Pro Leu Ile Ser Tyr Leu Leu Pro His Gln Asn Ala Thr Thr Ser Met	
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tta tct gat gac aac acc cca aaa tcc ata cat atc cct ttg ttg gac	1689
Leu Ser Asp Asp Asn Thr Pro Lys Ser Ile His Ile Pro Leu Leu Asp	
455 460 465	
caa gac tcg ttc att gag cct tca ggg aac cac aat gtg cct cgg cct	1737
Gln Asp Ser Phe Ile Glu Pro Ser Gly Asn His Asn Val Pro Arg Pro	
470 475 480	
gac agt ata cgt ggc ttc ttg aca cgg ccc act cga acc gtg cat tac	1785

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Tyr Trp Arg Gln Phe Asp Asp Ser Phe Met Arg Pro Val Phe Gly Gly
                               505                               510                               515

cgt ggc ttt gta ccc ttt gtt cca ggt tct cca act gag aga aac cct      1881
Arg Gly Phe Val Pro Phe Val Pro Gly Ser Pro Thr Glu Arg Asn Pro
                               520                               525                               530

cct gat ctt agt aag gct tgagggtaac gtggaagaaa agctttgatt          1929
Pro Asp Leu Ser Lys Ala
                               535

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Cys Ile Val Leu Gly His Leu Leu Glu Glu Asn Arg Trp Met Asn Glu
                               35                               40                               45

Ser Ile Thr Ala Leu Leu Ile Gly Leu Gly Thr Gly Val Thr Ile Leu
                               50                               55                               60

Leu Ile Ser Lys Gly Lys Ser Ser His Leu Leu Val Phe Ser Glu Asp
                               65                               70                               75                               80

Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala Gly Phe
                               85                               90                               95

Gln Val Lys Lys Lys Gln Phe Phe Arg Asn Phe Val Thr Ile Met Leu
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Phe	Gly	Ala	Val	Gly	Thr	Ile	Ile	Ser	Cys	Thr	Ile	Ile	Ser	Leu	Gly	115	120	125	
Val	Thr	Gln	Phe	Phe	Lys	Lys	Leu	Asp	Ile	Gly	Thr	Phe	Asp	Leu	Gly	130	135	140	
Asp	Tyr	Leu	Ala	Ile	Gly	Ala	Ile	Phe	Ala	Ala	Thr	Asp	Ser	Val	Cys	145	150	155	160
Thr	Leu	Gln	Val	Leu	Asn	Gln	Asp	Glu	Thr	Pro	Leu	Leu	Tyr	Ser	Leu	165	170	175	
Val	Phe	Gly	Glu	Gly	Val	Val	Asn	Asp	Ala	Thr	Ser	Val	Val	Val	Phe	180	185	190	
Asn	Ala	Ile	Gln	Ser	Phe	Asp	Leu	Thr	His	Leu	Asn	His	Glu	Ala	Ala	195	200	205	
Phe	His	Leu	Leu	Gly	Asn	Phe	Leu	Tyr	Leu	Phe	Leu	Leu	Ser	Thr	Leu	210	215	220	
Leu	Gly	Ala	Ala	Thr	Gly	Leu	Ile	Ser	Ala	Tyr	Val	Ile	Lys	Lys	Leu	225	230	235	240
Tyr	Phe	Gly	Arg	His	Ser	Thr	Asp	Arg	Glu	Val	Ala	Leu	Met	Met	Leu	245	250	255	
Met	Ala	Tyr	Leu	Ser	Tyr	Met	Leu	Ala	Glu	Leu	Phe	Asp	Leu	Ser	Gly	260	265	270	
Ile	Leu	Thr	Val	Phe	Phe	Cys	Gly	Ile	Val	Met	Ser	His	Tyr	Thr	Trp	275	280	285	
His	Asn	Val	Thr	Glu	Ser	Ser	Arg	Ile	Thr	Thr	Lys	His	Thr	Phe	Ala	290	295	300	
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Asp	Ala	Leu	Asp	Ile	Asp	Lys	Trp	Arg	Ser	Val	Ser	Asp	Thr	Pro	Gly	325	330	335	
Thr	Ser	Ile	Ala	Val	Ser	Ser	Ile	Leu	Met	Gly	Leu	Val	Met	Val	Gly	340	345	350	
Arg	Ala	Ala	Phe	Val	Phe	Pro	Leu	Ser	Phe	Leu	Ser	Asn	Leu	Ala	Lys	355	360	365	
Lys	Asn	Gln	Ser	Glu	Lys	Ile	Asn	Phe	Asn	Met	Gln	Val	Val	Ile	Trp	370	375	380	
Trp	Ser	Gly	Leu	Met	Arg	Gly	Ala	Val	Ser	Met	Ala	Leu	Ala	Tyr	Asn	385	390	395	400
Lys	Phe	Thr	Arg	Ala	Gly	His	Thr	Asp	Val	Arg	Gly	Asn	Ala	Ile	Met	405	410	415	

Ile Thr Ser Thr Ile Thr Val Cys Leu Phe Ser Thr Val Val Phe Gly
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Met Leu Thr Lys Pro Leu Ile Ser Tyr Leu Leu Pro His Gln Asn Ala
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Thr Thr Ser Met Leu Ser Asp Asp Asn Thr Pro Lys Ser Ile His Ile
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Pro Leu Leu Asp Gln Asp Ser Phe Ile Glu Pro Ser Gly Asn His Asn
465 470 475 480

Val Pro Arg Pro Asp Ser Ile Arg Gly Phe Leu Thr Arg Pro Thr Arg
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Thr Val His Tyr Tyr Trp Arg Gln Phe Asp Asp Ser Phe Met Arg Pro
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His Pro Gln Val Ile Pro Ile Ser Val Phe Ile Ala Ile Leu Cys Leu
20 25 30

tgt tta gtt atc ggc cac ttg ctt gaa gag aat cga tgg gtt aat gaa 204
Cys Leu Val Ile Gly His Leu Leu Glu Glu Asn Arg Trp Val Asn Glu
35 40 45

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Ser Ile Thr Ala Ile Leu Val Gly Ala Ala Ser Gly Thr Val Ile Leu
50 55 60

ctt att agt aaa gga aaa agt tca cat att ttg gtg ttt gat gaa gaa 300
Leu Ile Ser Lys Gly Lys Ser Ser His Ile Leu Val Phe Asp Glu Glu

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Gln Val Lys Lys Lys Lys Phe Phe His Asn Phe Leu Thr Ile Met Ser	100	105	110	
ttt ggt gtg att gga gtt ttc atc tcc act gtc att atc tcg ttt ggg				444
Phe Gly Val Ile Gly Val Phe Ile Ser Thr Val Ile Ile Ser Phe Gly	115	120	125	
act tgg tgg ctg ttt ccc aag ttg gga ttt aag ggg ttg agt gct aga				492
Thr Trp Trp Leu Phe Pro Lys Leu Gly Phe Lys Gly Leu Ser Ala Arg	130	135	140	
gac tat ctt gcc ata gga acg att ttc tca tca act gat act gtt tgc				540
Asp Tyr Leu Ala Ile Gly Thr Ile Phe Ser Ser Thr Asp Thr Val Cys	145	150	155	160
act cta cag att ctc cat caa gat gaa aca cca ttg cta tac agc tta				588
Thr Leu Gln Ile Leu His Gln Asp Glu Thr Pro Leu Leu Tyr Ser Leu	165	170	175	
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Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Val Val Leu Phe	180	185	190	
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Asn Ala Val Gln Lys Ile Gln Phe Glu Ser Leu Thr Gly Trp Thr Ala	195	200	205	
ctg caa gta ttt ggg aac ttt ttg tac ctc ttc tca aca agc aca ctt				732
Leu Gln Val Phe Gly Asn Phe Leu Tyr Leu Phe Ser Thr Ser Thr Leu	210	215	220	
ctc gga att ggt gtg ggg cta ata aca tct ttt gtt ctt aaa acc ttg				780
Leu Gly Ile Gly Val Gly Leu Ile Thr Ser Phe Val Leu Lys Thr Leu	225	230	235	240
tat ttt gga aga cat tct act aca cgc gaa ctc gcc atc atg gtt cta				828
Tyr Phe Gly Arg His Ser Thr Thr Arg Glu Leu Ala Ile Met Val Leu	245	250	255	
atg gct tac ctt tca tat atg ttg gct gag ctc ttc tca tta agt gga				876
Met Ala Tyr Leu Ser Tyr Met Leu Ala Glu Leu Phe Ser Leu Ser Gly	260	265	270	
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Ile Leu Thr Val Phe Phe Cys Gly Val Leu Met Ser His Tyr Ala Ser	275	280	285	
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Tyr Asn Val Thr Glu Ser Ser Arg Ile Thr Ser Arg His Val Phe Ala	290	295	300	

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Met Leu Ser Phe Ile Ala Glu Thr Phe Ile Phe Leu Tyr Val Gly Thr	
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515 520 525	

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35 40 45

Ser Ile Thr Ala Ile Leu Val Gly Ala Ala Ser Gly Thr Val Ile Leu
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Ala Ala Gly Ile Arg Gly Arg Leu Gly His Val Leu Arg Arg His Arg
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Phe His Tyr Leu Pro Glu Ala Ser Gly Ser Leu Leu Ile Gly Leu Ile
      20                      25                      30

gtc ggt ata ctt gct aat atc tcc gat act gag act agc att agg acg 201
Val Gly Ile Leu Ala Asn Ile Ser Asp Thr Glu Thr Ser Ile Arg Thr
      35                      40                      45

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Trp Phe Asn Phe His Glu Glu Phe Phe Phe Leu Phe Leu Leu Pro Pro
      50                      55                      60                      65

atc ata ttc cag tca ggt ttc agt ctt caa cct aaa cca ttc ttt tct 297
Ile Ile Phe Gln Ser Gly Phe Ser Leu Gln Pro Lys Pro Phe Phe Ser
      70                      75                      80

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Asn Phe Gly Ala Ile Val Thr Phe Ala Ile Ile Gly Thr Phe Val Ala
      85                      90                      95

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Ser Val Val Thr Gly Gly Leu Val Tyr Leu Gly Gly Ser Met Tyr Leu
      100                      105                      110

atg tat aaa ctt ccc ttt gtt gag tgt ctt atg ttt ggt gca ctt ata 441
Met Tyr Lys Leu Pro Phe Val Glu Cys Leu Met Phe Gly Ala Leu Ile
      115                      120                      125

tca gct acg gac cct gtc act gta ctc tct ata ttc cag gat gtg ggc 489
Ser Ala Thr Asp Pro Val Thr Val Leu Ser Ile Phe Gln Asp Val Gly

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130                      135                      140                      145
acc gat gtt aac ctg tat gct ttg gtc ttt gga gaa tca gtt ctg aat 537
Thr Asp Val Asn Leu Tyr Ala Leu Val Phe Gly Glu Ser Val Leu Asn
                      150                      155                      160

gat gct atg gca ata tca ttg tac aga aca atg tcc tta gta aac cgc 585
Asp Ala Met Ala Ile Ser Leu Tyr Arg Thr Met Ser Leu Val Asn Arg
                      165                      170                      175

cag tcc tcg tct ggg gaa cat ttt tca tgggtggatg cagggtttttt 632
Gln Ser Ser Ser Ser Gly Glu His Phe Ser
                      180                      185

gagacttttgc tgggtcaatg tcgcaggggt tgggggttggga ttcacttcag cttaatatcc 692

tcctcgatcc tcctatttcc ta 714

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<210> 6
<211> 186
<212> PRT
<213> Arabidopsis thaliana

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<220>
<223> Figure 1(c) (i)

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<400> 6

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 1              5              10              15

Arg Phe His Tyr Leu Pro Glu Ala Ser Gly Ser Leu Leu Ile Gly Leu
          20              25              30

Ile Val Gly Ile Leu Ala Asn Ile Ser Asp Thr Glu Thr Ser Ile Arg
      35              40              45

Thr Trp Phe Asn Phe His Glu Glu Phe Phe Phe Leu Phe Leu Leu Pro
      50              55              60

Pro Ile Ile Phe Gln Ser Gly Phe Ser Leu Gln Pro Lys Pro Phe Phe
      65              70              75              80

Ser Asn Phe Gly Ala Ile Val Thr Phe Ala Ile Ile Gly Thr Phe Val
          85              90              95

Ala Ser Val Val Thr Gly Gly Leu Val Tyr Leu Gly Gly Ser Met Tyr
          100              105              110

Leu Met Tyr Lys Leu Pro Phe Val Glu Cys Leu Met Phe Gly Ala Leu
      115              120              125

Ile Ser Ala Thr Asp Pro Val Thr Val Leu Ser Ile Phe Gln Asp Val
      130              135              140

Gly Thr Asp Val Asn Leu Tyr Ala Leu Val Phe Gly Glu Ser Val Leu

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145		150		155		160
Asn Asp Ala Met	Ala Ile Ser Leu Tyr Arg Thr Met Ser Leu Val Asn					
	165		170		175	

Arg Gln Ser	Ser Ser Gly Glu His Phe Ser
180	185

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 <213> Arabidopsis thaliana

<220>
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 <222> (52)..(393)
 <223> Figure 1(c)(ii)

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Gly His Gly Pro Ile Ile Phe Tyr Cys Thr Thr Thr Ile Val Val Val	
5 10 15	
acg gtt tta cta ata gga ggt tcg aca ggt aaa atg ttg gaa gct ttg	153
Thr Val Leu Leu Ile Gly Gly Ser Thr Gly Lys Met Leu Glu Ala Leu	
20 25 30	
gaa gtt gta ggt gac gat ctt gat gac tcc atg tct gaa ggc ttt gaa	201
Glu Val Val Gly Asp Asp Leu Asp Asp Ser Met Ser Glu Gly Phe Glu	
35 40 45 50	
gag agc gat cat cag tat gtc cct cct cct ttt agc att gga gct tca	249
Glu Ser Asp His Gln Tyr Val Pro Pro Pro Phe Ser Ile Gly Ala Ser	
55 60 65	
tct gac gag gat aca tca tca tca gga agc agg ttc aag atg aag ctg	297
Ser Asp Glu Asp Thr Ser Ser Ser Gly Ser Arg Phe Lys Met Lys Leu	
70 75 80	
aag gag ttt cac aaa acc act aca tca ttc acc gcg ttg gac aaa aac	345
Lys Glu Phe His Lys Thr Thr Thr Ser Phe Thr Ala Leu Asp Lys Asn	
85 90 95	
ttt ctg act ccg ttc ttc aca act aat agt gga gat gga gat gga gat	393
Phe Leu Thr Pro Phe Phe Thr Thr Asn Ser Gly Asp Gly Asp Gly Asp	
100 105 110	
ggggagtagc atggaaaaga tgtgtat	420

<210> 8

<211> 114
 <212> PRT
 <213> Arabidopsis thaliana

<220>
 <223> Figure 1(c)(ii)

<400> 8

Thr	Arg	Gly	His	Gly	Pro	Ile	Ile	Phe	Tyr	Cys	Thr	Thr	Thr	Ile	Val
1				5					10					15	
Val	Val	Thr	Val	Leu	Leu	Ile	Gly	Gly	Ser	Thr	Gly	Lys	Met	Leu	Glu
			20					25					30		
Ala	Leu	Glu	Val	Val	Gly	Asp	Asp	Leu	Asp	Asp	Ser	Met	Ser	Glu	Gly
		35					40					45			
Phe	Glu	Glu	Ser	Asp	His	Gln	Tyr	Val	Pro	Pro	Pro	Phe	Ser	Ile	Gly
	50					55					60				
Ala	Ser	Ser	Asp	Glu	Asp	Thr	Ser	Ser	Ser	Gly	Ser	Arg	Phe	Lys	Met
	65				70					75					80
Lys	Leu	Lys	Glu	Phe	His	Lys	Thr	Thr	Thr	Ser	Phe	Thr	Ala	Leu	Asp
				85					90					95	
Lys	Asn	Phe	Leu	Thr	Pro	Phe	Phe	Thr	Thr	Asn	Ser	Gly	Asp	Gly	Asp
			100					105					110		

Gly Asp

<210> 9
 <211> 2284
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <223> Figure 5(a) and (b)

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 gtcccgtaat tttctccttt tttttcttcc ccaattcctt caattttcga attcgctct 120
 ctgtttcggt cctcgtagac gaagaagaag aagaatctca ggtttttagct ttcgaagctt 180
 ccaaaatttt gaattttgat cttctgggct cttttgtaaa tcagactgaa gatattttaga 240
 ttaccagaa gttgttcaag gaatgggttc agtggacagc acggaaagat aaaagagact 300
 tttttttcca gattttgctg atccaaaatc tgaatagttg ttcattgtct tggatcaa 360
 ctggaaagag gaagtttggt ggatctagaa gaagataaca atgttggtt ctctagtgtc 420

gaaactgcct tcgttatcga catctgatca cgcttctgtg gttgcgttga atctctttgt 480
tgcacttctt tgtgcttgta ttgttcttgg tcactctttg gaagagaata gatggatgaa 540
cgaatccatc accgccttgt tgattgggct aggcactggg gttaccattt tgttgattag 600
taaaggaaaa agctcgcac tctctgtctt tagtgaagat cttttcttca tatactcttt 660
gccaccatt atattcaatg cagggtttca agtaaaaaag aagcagtttt tccgcaattt 720
cgtgactatt atgctttttg gtgctgttgg gactattatt tcttgacaaa tcatatctct 780
aggtgtaaca cagttcttta agaagttgga cattggaacc tttgacttgg gtgattatct 840
tgctattggg gccatatttg ctgcaacaga ttcagtatgt aactgcagg ttctgaatca 900
agacgagaca cctttgcttt acagtcttgt attcggagag ggtgttgtga atgatgcaac 960
gtcagttgtg gtcttcaacg cgattcagag ctttgatctc actcacctaa accacgaagc 1020
tgcttttcat cttcttgga acttcttgta tttgtttctc ctaagtacct tgcttgggtc 1080
tgcaaccggg ctgataagtg cgtatgttat caagaagcta tactttggaa ggcactcaac 1140
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tttcgacttg agcggtatcc tcaactgtgtt tttctgtggg attgtgatgt cccattacac 1260
atggcacaat gtaacggaga gctcaagaat aacaacaaag catacctttg caactttgtc 1320
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caagaagaat caaagcgaga aaatcaactt taacatgcag gttgtgattt ggtgggtctgg 1560
tctcatgaga ggtgctgtat ctatggctct tgcatacaac aagtttaciaa gggccgggca 1620
cacagatgta cgcgggaatg caatcatgat cagagtagc ataactgtct gtcttttttag 1680
cacagtgggtg tttgggtatgc tgaccaaacc actcataagc tacctattac cgcaccagaa 1740
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ggaccaagac tcgttcattg agccttcagg gaaccacaat gtgcctcggc ctgacagtat 1860
acgtggcttc ttgacacggc ccaactcgaa ccgtgcatta ctaactggag acaatttgat 1920
gactctttca tgcgaccgt ctttgagggt cgtggctttg taccctttgt tccaggttct 1980
ccaactgaga gaaaccctcc tgatcttagt aaggcttgag ggtaacgtgg aagaaaagct 2040
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gtaatattgt ttgtgaggac agaaatctgt cctaacgttt tgagagcaga aagcaaaaca 2160
 tggcaacttt gaagtgtttg attgatgtat gtaattatat tcatatttgt tttgttgtaa 2220
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 aaaa 2284

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 <212> PRT
 <213> Arabidopsis thaliana

<220>
 <223> Figure 5(a)and (b)

<400> 10

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His	Ala	Ser	Val	Val	Ala	Leu	Asn	Leu	Phe	Val	Ala	Leu	Leu	Cys	Ala	20	25	30	
Cys	Ile	Val	Leu	Gly	His	Leu	Leu	Glu	Glu	Asn	Arg	Trp	Met	Asn	Glu	35	40	45	
Ser	Ile	Thr	Ala	Leu	Leu	Ile	Gly	Leu	Gly	Thr	Gly	Val	Thr	Ile	Leu	50	55	60	
Leu	Ile	Ser	Lys	Gly	Lys	Ser	Ser	His	Leu	Leu	Val	Phe	Ser	Glu	Asp	65	70	75	80
Leu	Phe	Phe	Ile	Tyr	Leu	Leu	Pro	Pro	Ile	Ile	Phe	Asn	Ala	Gly	Phe	85	90	95	
Gln	Val	Lys	Lys	Lys	Gln	Phe	Phe	Arg	Asn	Phe	Val	Thr	Ile	Met	Leu	100	105	110	
Phe	Gly	Ala	Val	Gly	Thr	Ile	Ile	Ser	Cys	Thr	Ile	Ile	Ser	Leu	Gly	115	120	125	
Val	Thr	Gln	Phe	Phe	Lys	Lys	Leu	Asp	Ile	Gly	Thr	Phe	Asp	Leu	Gly	130	135	140	
Asp	Tyr	Leu	Ala	Ile	Gly	Ala	Ile	Phe	Ala	Ala	Thr	Asp	Ser	Val	Cys	145	150	155	160
Thr	Leu	Gln	Val	Leu	Asn	Gln	Asp	Glu	Thr	Pro	Leu	Leu	Tyr	Ser	Leu	165	170	175	
Val	Phe	Gly	Glu	Gly	Val	Val	Asn	Asp	Ala	Thr	Ser	Val	Val	Val	Phe	180	185	190	
Asn	Ala	Ile	Gln	Ser	Phe	Asp	Leu	Thr	His	Leu	Asn	His	Glu	Ala	Ala	195	200	205	

Phe His Leu Leu Gly Asn Phe Leu Tyr Leu Phe Leu Leu Ser Thr Leu
210 215 220
Leu Gly Ala Ala Thr Gly Leu Ile Ser Ala Tyr Val Ile Lys Lys Leu
225 230 235 240
Tyr Phe Gly Arg His Ser Thr Asp Arg Glu Val Ala Leu Met Met Leu
245 250 255
Met Ala Tyr Leu Ser Tyr Met Leu Ala Glu Leu Phe Asp Leu Ser Gly
260 265 270
Ile Leu Thr Val Phe Phe Cys Gly Ile Val Met Ser His Tyr Thr Trp
275 280 285
His Asn Val Thr Glu Ser Ser Arg Ile Thr Thr Lys His Thr Phe Ala
290 295 300
Thr Leu Ser Phe Leu Ala Glu Thr Phe Ile Phe Leu Tyr Val Gly Met
305 310 315 320
Asp Ala Leu Asp Ile Asp Lys Trp Arg Ser Val Ser Asp Thr Pro Gly
325 330 335
Thr Ser Ile Ala Val Ser Ser Ile Leu Met Gly Leu Val Met Val Gly
340 345 350
Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn Leu Ala Lys
355 360 365
Lys Asn Gln Ser Glu Lys Ile Asn Phe Asn Met Gln Val Val Ile Trp
370 375 380
Trp Ser Gly Leu Met Arg Gly Ala Val Ser Met Ala Leu Ala Tyr Asn
385 390 395 400
Lys Phe Thr Arg Ala Gly His Thr Asp Val Arg Gly Asn Ala Ile Met
405 410 415
Ile Thr Ser Thr Ile Thr Val Cys Leu Phe Ser Thr Val Val Phe Gly
420 425 430
Met Leu Thr Lys Pro Leu Ile Ser Tyr Leu Leu Pro His Gln Asn Ala
435 440 445
Thr Thr Ser Met Leu Ser Asp Asp Asn Thr Pro Lys Ser Ile His Ile
450 455 460
Pro Leu Leu Asp Gln Asp Ser Phe Ile Glu Pro Ser Gly Asn His Asn
465 470 475 480
Val Pro Arg Pro Asp Ser Ile Arg Gly Phe Leu Thr Arg Pro Thr Arg
485 490 495
Asn Arg Ala Leu Leu Thr Gly Asp Asn Leu Met Thr Leu Ser Cys Asp
500 505 510

Pro Ser Leu Glu Val Val Ala Leu Tyr Pro Leu Phe Gln Val Leu Gln
515 520 525

Leu Arg Glu Thr Leu Leu Ile Leu Val Arg Leu Glu Gly Asn Val Glu
530 535 540

Glu Lys Leu
545

<210> 11
<211> 24
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<213> Synthetic

<220>
<223> Page 5 and 53 - Forward primer - Isolated
oligonucleotide sequence

<400> 11

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24

<210> 12
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<212> DNA
<213> Synthetic

<220>
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oligonucleotide

<400> 12

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27

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<220>
<223> Pages 5 and 53 - Isolated oligonucleotide

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29

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<220>
<223> Page 5 - Isolated oligonucleotide

<400> 14

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<210> 15
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<220>
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<400> 15

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<210> 16
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<220> <221> CDS
<222> (67)..(1041)
<223> Figure 1(d)

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cagatt atg atg ctc gtg ctt tcc ttc gtt ctc ggc cat gtc ctc cgc 108
Met Met Leu Val Leu Ser Phe Val Leu Gly His Val Leu Arg
1 5 10

cgt cat cga ttc cac tat ctt cct gaa gcc agc ggt tcg ctt ctc att 156
Arg His Arg Phe His Tyr Leu Pro Glu Ala Ser Gly Ser Leu Leu Ile
15 20 25 30

ggg tta atc gtc ggt ata ctt gct aat atc tcc gat act gag act agc 204
Gly Leu Ile Val Gly Ile Leu Ala Asn Ile Ser Asp Thr Glu Thr Ser

	35	40	45	
att agg acg tgg ttt aat ttc cac gaa gag ttc ttc ttc ttg ttt ttg				252
Ile Arg Thr Trp Phe Asn Phe His Glu Glu Phe Phe Phe Leu Phe Leu				
	50	55	60	
ttg cct ccc atc ata ttc cag tca ggt ttc agt ctt caa cct aaa cca				300
Leu Pro Pro Ile Ile Phe Gln Ser Gly Phe Ser Leu Gln Pro Lys Pro				
	65	70	75	
ttc ttt tct aac ttt gga gcc att gtt acc ttt gct atc atc gga act				348
Phe Phe Ser Asn Phe Gly Ala Ile Val Thr Phe Ala Ile Ile Gly Thr				
	80	85	90	
ttt gtc gct tca gtt gtt act ggt ggt ctg gtt tat ctt ggc ggc tct				396
Phe Val Ala Ser Val Val Thr Gly Gly Leu Val Tyr Leu Gly Gly Ser				
	95	100	105	110
atg tat ctc atg tat aaa ctt ccc ttt gtt gag tgt ctt atg ttt ggt				444
Met Tyr Leu Met Tyr Lys Leu Pro Phe Val Glu Cys Leu Met Phe Gly				
	115	120	125	
gca ctt ata tca gct acg gac cct gtc act gta ctc tct ata ttc cag				492
Ala Leu Ile Ser Ala Thr Asp Pro Val Thr Val Leu Ser Ile Phe Gln				
	130	135	140	
gat gtg ggc acc gat gtt aac ctg tat gct ttg gtc ttt gga gaa tca				540
Asp Val Gly Thr Asp Val Asn Leu Tyr Ala Leu Val Phe Gly Glu Ser				
	145	150	155	
gtt ctg aat gat gct atg gca ata tca ttg tac aga aca atg tcc tta				588
Val Leu Asn Asp Ala Met Ala Ile Ser Leu Tyr Arg Thr Met Ser Leu				
	160	165	170	
gta aac cgc cag tcc tcg tct ggg gaa cat ttt ttc atg gtg gtg atc				636
Val Asn Arg Gln Ser Ser Ser Gly Glu His Phe Phe Met Val Val Ile				
	175	180	185	190
agg ttt ttt gag act ttt gct ggc tca atg tct gca ggg gtt ggg gtt				684
Arg Phe Phe Glu Thr Phe Ala Gly Ser Met Ser Ala Gly Val Gly Val				
	195	200	205	
gga ttc act tca gct tta ctc ttt aag tat gca gga ttg gac acc gag				732
Gly Phe Thr Ser Ala Leu Leu Phe Lys Tyr Ala Gly Leu Asp Thr Glu				
	210	215	220	
aat ctt cag aac ttg gag tgt tgt ctc ttt gta ctt ttc ccg tat ttt				780
Asn Leu Gln Asn Leu Glu Cys Cys Leu Phe Val Leu Phe Pro Tyr Phe				
	225	230	235	
tca tac atg ctt gca gaa ggt gtt ggt ctc tcc ggc att gtt tct ata				828
Ser Tyr Met Leu Ala Glu Gly Val Gly Leu Ser Gly Ile Val Ser Ile				
	240	245	250	
ctc ttc aca gga att gtt atg aag cgc tac act ttc tca aat ctc tca				876
Leu Phe Thr Gly Ile Val Met Lys Arg Tyr Thr Phe Ser Asn Leu Ser				
	255	260	265	270

gaa gct tca cag agt ttc gta tct tct ttt ttt cac ttg ata tct tcg 924
 Glu Ala Ser Gln Ser Phe Val Ser Ser Phe Phe His Leu Ile Ser Ser
 275 280 285

 cta gca gaa act ttc acg ttc att tac atg gga ttt gat att gcc atg 972
 Leu Ala Glu Thr Phe Thr Phe Ile Tyr Met Gly Phe Asp Ile Ala Met
 290 295 300

 gag cag cat agc tgg tcc cat gtt ggg ttt atc ctt ttc tct att gta 1020
 Glu Gln His Ser Trp Ser His Val Gly Phe Ile Leu Phe Ser Ile Val
 305 310 315

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 Ser Ser Phe Thr Asp Arg Gln
 320 325

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<212> PRT

<213> *Arabidopsis thaliana*

<220>

<223> Figure 1(d)

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 20 25 30

Ile Val Gly Ile Leu Ala Asn Ile Ser Asp Thr Glu Thr Ser Ile Arg

35					40					45						
Thr	Trp	Phe	Asn	Phe	His	Glu	Glu	Phe	Phe	Phe	Leu	Phe	Leu	Leu	Pro	
50					55					60						
Pro	Ile	Ile	Phe	Gln	Ser	Gly	Phe	Ser	Leu	Gln	Pro	Lys	Pro	Phe	Phe	
65					70					75					80	
Ser	Asn	Phe	Gly	Ala	Ile	Val	Thr	Phe	Ala	Ile	Ile	Gly	Thr	Phe	Val	
85					90					95						
Ala	Ser	Val	Val	Thr	Gly	Gly	Leu	Val	Tyr	Leu	Gly	Gly	Ser	Met	Tyr	
100					105					110						
Leu	Met	Tyr	Lys	Leu	Pro	Phe	Val	Glu	Cys	Leu	Met	Phe	Gly	Ala	Leu	
115					120					125						
Ile	Ser	Ala	Thr	Asp	Pro	Val	Thr	Val	Leu	Ser	Ile	Phe	Gln	Asp	Val	
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165					170					175						
Arg	Gln	Ser	Ser	Ser	Gly	Glu	His	Phe	Phe	Met	Val	Val	Ile	Arg	Phe	
180					185					190						
Phe	Glu	Thr	Phe	Ala	Gly	Ser	Met	Ser	Ala	Gly	Val	Gly	Val	Gly	Phe	
195					200					205						
Thr	Ser	Ala	Leu	Leu	Phe	Lys	Tyr	Ala	Gly	Leu	Asp	Thr	Glu	Asn	Leu	
210					215					220						
Gln	Asn	Leu	Glu	Cys	Cys	Leu	Phe	Val	Leu	Phe	Pro	Tyr	Phe	Ser	Tyr	
225					230					235					240	
Met	Leu	Ala	Glu	Gly	Val	Gly	Leu	Ser	Gly	Ile	Val	Ser	Ile	Leu	Phe	
245					250					255						
Thr	Gly	Ile	Val	Met	Lys	Arg	Tyr	Thr	Phe	Ser	Asn	Leu	Ser	Glu	Ala	
260					265					270						
Ser	Gln	Ser	Phe	Val	Ser	Ser	Phe	Phe	His	Leu	Ile	Ser	Ser	Leu	Ala	
275					280					285						
Glu	Thr	Phe	Thr	Phe	Ile	Tyr	Met	Gly	Phe	Asp	Ile	Ala	Met	Glu	Gln	
290					295					300						
His	Ser	Trp	Ser	His	Val	Gly	Phe	Ile	Leu	Phe	Ser	Ile	Val	Ser	Ser	
305					310					315					320	
Phe	Thr	Asp	Arg	Gln												
325																

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 <212> DNA
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 <222> (55)..(750)
 <223> Figure 1(e) AtNHX4 CDNA sequence

<400> 19

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Met Leu Val Leu Ser Phe Val Leu Gly His Val Leu Arg Arg His Arg
      5                      10                      15

ttc cac tat ctt cct gaa gcc agc ggt tcg ctt ctc att ggt tta atc 153
Phe His Tyr Leu Pro Glu Ala Ser Gly Ser Leu Leu Ile Gly Leu Ile
      20                      25                      30

gtc ggt ata ctt gct aat atc tcc gat act gag act agc att agg acg 201
Val Gly Ile Leu Ala Asn Ile Ser Asp Thr Glu Thr Ser Ile Arg Thr
      35                      40                      45

tgg ttt aat ttc cac gaa gag ttc ttc ttc ttg ttt ttg ttg cct ccc 249
Trp Phe Asn Phe His Glu Glu Phe Phe Phe Leu Phe Leu Leu Pro Pro
      50                      55                      60                      65

atc ata ttc cag tca ggt ttc agt ctt caa cct aaa cca ttc ttt tct 297
Ile Ile Phe Gln Ser Gly Phe Ser Leu Gln Pro Lys Pro Phe Phe Ser
      70                      75                      80

aac ttt gga gcc att gtt acc ttt gct atc atc gga act ttt gtc gct 345
Asn Phe Gly Ala Ile Val Thr Phe Ala Ile Ile Gly Thr Phe Val Ala
      85                      90                      95

tca gtt gtt act ggt ggt ctg gtt tat ctt ggc ggc tct atg tat ctc 393
Ser Val Val Thr Gly Gly Leu Val Tyr Leu Gly Gly Ser Met Tyr Leu
      100                      105                      110

atg tat aaa ctt ccc ttt gtt gag tgt ctt atg ttt ggt gca ctt ata 441
Met Tyr Lys Leu Pro Phe Val Glu Cys Leu Met Phe Gly Ala Leu Ile
      115                      120                      125

tca gct acg gac cct gtc act gta ctc tct ata ttc cag gat gtg ggc 489
Ser Ala Thr Asp Pro Val Thr Val Leu Ser Ile Phe Gln Asp Val Gly
      130                      135                      140                      145

acc gat gtt aac ctg tat gct ttg gtc ttt gga gaa tca gtt ctg aat 537
Thr Asp Val Asn Leu Tyr Ala Leu Val Phe Gly Glu Ser Val Leu Asn
      150                      155                      160

gat gct atg gca ata tca ttg tac aga aca atg tcc tta gta aac cgc 585

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[illegible]

acaaaaactt tctgactccg ttcttcacaa ctaatagtgg agatggagat ggagatgggg 1980
 agtagcatgg aaaagatgtg tatttgtggg ccaggccaag ctataattag agtacacata 2040
 tgtctatgta agattaacac tggttgattt tacctctcgc aaaatgccca ctataaagtt 2100
 gacgatttcc aagacatttc ga 2122

<210> 20
 <211> 232
 <212> PRT
 <213> Arabidopsis thaliana

<220>
 <223> Figure 1(e)

<400> 20

Met	Met	Leu	Val	Leu	Ser	Phe	Val	Leu	Gly	His	Val	Leu	Arg	Arg	His
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Arg	Phe	His	Tyr	Leu	Pro	Glu	Ala	Ser	Gly	Ser	Leu	Leu	Ile	Gly	Leu
			20					25					30		
Ile	Val	Gly	Ile	Leu	Ala	Asn	Ile	Ser	Asp	Thr	Glu	Thr	Ser	Ile	Arg
		35					40					45			
Thr	Trp	Phe	Asn	Phe	His	Glu	Glu	Phe	Phe	Phe	Leu	Phe	Leu	Leu	Pro
	50					55					60				
Pro	Ile	Ile	Phe	Gln	Ser	Gly	Phe	Ser	Leu	Gln	Pro	Lys	Pro	Phe	Phe
65					70					75					80
Ser	Asn	Phe	Gly	Ala	Ile	Val	Thr	Phe	Ala	Ile	Ile	Gly	Thr	Phe	Val
				85					90					95	
Ala	Ser	Val	Val	Thr	Gly	Gly	Leu	Val	Tyr	Leu	Gly	Gly	Ser	Met	Tyr
			100					105					110		
Leu	Met	Tyr	Lys	Leu	Pro	Phe	Val	Glu	Cys	Leu	Met	Phe	Gly	Ala	Leu
		115					120					125			
Ile	Ser	Ala	Thr	Asp	Pro	Val	Thr	Val	Leu	Ser	Ile	Phe	Gln	Asp	Val
	130					135					140				
Gly	Thr	Asp	Val	Asn	Leu	Tyr	Ala	Leu	Val	Phe	Gly	Glu	Ser	Val	Leu
145				150						155					160
Asn	Asp	Ala	Met	Ala	Ile	Ser	Leu	Tyr	Arg	Thr	Met	Ser	Leu	Val	Asn
			165						170					175	
Arg	Gln	Ser	Ser	Ser	Gly	Glu	His	Phe	Phe	Met	Val	Val	Ile	Arg	Phe
		180						185					190		
Phe	Glu	Thr	Phe	Ala	Gly	Ser	Met	Ser	Ala	Gly	Val	Gly	Val	Gly	Phe
		195					200					205			

Thr Ser Ala Leu Ile Ser Phe Leu Glu Ser Ser Ile Phe Leu Ile Arg
 210 215 220

Cys His Met Ala Lys Asn Val Leu
 225 230

<210> 21
 <211> 569
 <212> PRT
 <213> Schizosaccharomyces pombe

<220>
 <223> Figure 8(a)

<400> 21

Met Pro Asp Ser Lys His Trp Val Ile Leu Leu Phe Arg Arg Asp Gly
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 Asp Asp Asp Asp Asp Asp Gly Gln Asp Pro Ala Leu Gln Glu Leu Tyr
 20 25 30
 Ser Ser Trp Ala Leu Phe Ile Leu Leu Val Leu Leu Ile Gly Ala Leu
 35 40 45
 Leu Thr Ser Tyr Tyr Val Gln Ser Lys Lys Ile Arg Ala Ile His Glu
 50 55 60
 Thr Val Ile Ser Val Phe Val Gly Met Val Val Gly Leu Ile Ile Arg
 65 70 75 80
 Val Ser Pro Gly Leu Ile Ile Gln Asn Met Val Ser Phe His Ser Thr
 85 90 95
 Tyr Phe Phe Asn Val Leu Leu Pro Pro Ile Ile Leu Asn Ser Gly Tyr
 100 105 110
 Glu Leu His Gln Ser Asn Phe Phe Arg Asn Ile Gly Thr Ile Leu Thr
 115 120 125
 Phe Ala Phe Ala Gly Thr Phe Ile Ser Ala Val Thr Leu Gly Val Leu
 130 135 140
 Val Tyr Ile Phe Ser Phe Leu Asn Phe Glu Asn Leu Ser Met Thr Phe
 145 150 155 160
 Val Glu Ala Leu Ser Met Gly Ala Thr Leu Ser Ala Thr Asp Pro Val
 165 170 175
 Thr Val Leu Ala Ile Phe Asn Ser Tyr Lys Val Asp Gln Lys Leu Tyr
 180 185 190
 Thr Ile Ile Phe Gly Glu Ser Ile Leu Asn Asp Ala Val Ala Ile Val
 195 200 205

Met	Phe	Glu	Thr	Leu	Gln	Gln	Phe	Gln	Gly	Lys	Thr	Leu	His	Phe	Phe	
210						215					220					
Thr	Leu	Phe	Ser	Gly	Ile	Gly	Ile	Phe	Ile	Ile	Thr	Phe	Phe	Ile	Ser	
225					230					235					240	
Leu	Leu	Ile	Gly	Val	Ser	Ile	Gly	Leu	Ile	Thr	Ala	Leu	Leu	Leu	Lys	
				245					250					255		
Tyr	Ser	Tyr	Leu	Arg	Arg	Tyr	Pro	Ser	Ile	Glu	Ser	Cys	Ile	Ile	Leu	
			260					265					270			
Leu	Met	Ala	Tyr	Thr	Ser	Tyr	Phe	Phe	Ser	Asn	Gly	Cys	His	Met	Ser	
		275					280					285				
Gly	Val	Val	Ser	Leu	Leu	Phe	Cys	Gly	Ile	Thr	Leu	Lys	His	Tyr	Ala	
	290					295					300					
Phe	Phe	Asn	Met	Ser	Tyr	Lys	Ala	Lys	Leu	Ser	Thr	Lys	Tyr	Val	Phe	
305					310					315					320	
Arg	Val	Leu	Ala	Gln	Leu	Ser	Glu	Asn	Phe	Ile	Phe	Ile	Tyr	Leu	Gly	
				325					330					335		
Met	Ser	Leu	Phe	Thr	Gln	Val	Asp	Leu	Val	Tyr	Lys	Pro	Ile	Phe	Ile	
			340					345					350			
Leu	Ile	Thr	Thr	Val	Ala	Val	Thr	Ala	Ser	Arg	Tyr	Met	Asn	Val	Phe	
		355					360					365				
Pro	Leu	Ser	Asn	Leu	Leu	Asn	Lys	Phe	His	Arg	Gln	Arg	Asn	Gly	Asn	
	370					375					380					
Leu	Ile	Asp	His	Ile	Pro	Tyr	Ser	Tyr	Gln	Met	Met	Leu	Phe	Trp	Ala	
385					390					395					400	
Gly	Leu	Arg	Gly	Ala	Val	Gly	Val	Ala	Leu	Ala	Ala	Gly	Phe	Glu	Gly	
				405					410					415		
Glu	Asn	Ala	Gln	Thr	Leu	Arg	Ala	Thr	Thr	Leu	Val	Val	Val	Val	Leu	
			420					425					430			
Thr	Leu	Ile	Ile	Phe	Gly	Gly	Thr	Thr	Ala	Arg	Met	Leu	Glu	Ile	Leu	
		435					440					445				
His	Ile	Glu	Thr	Gly	Val	Ala	Ala	Asp	Val	Asp	Ser	Asp	Thr	Glu	Ile	
	450					455					460					
Gly	Met	Leu	Pro	Trp	Gln	Gln	Ser	Pro	Glu	Phe	Asp	Leu	Glu	Asn	Ser	
465					470					475					480	
Ala	Met	Glu	Leu	Ser	Asp	Ala	Ser	Ala	Glu	Pro	Val	Val	Val	Asp	Gln	
				485					490					495		
Gln	Phe	Thr	Thr	Glu	His	Phe	Asp	Glu	Gly	Asn	Ile	Ala	Pro	Thr	Leu	
			500					505					510			

Ser Lys Lys Val Ser Ser Thr Phe Glu Gln Tyr Gln Arg Ala Ala Gly
515 520 525

Ala Phe Asn Gln Phe Phe His Ser Ser Arg Asp Asp Gln Ala Gln Trp
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Leu Thr Arg Phe Asp Glu Glu Val Ile Lys Pro Val Leu Leu Glu Arg
545 550 555 560

Asp Asn Leu Lys Asn Gly Thr Lys Lys
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<210> 22
<211> 633
<212> PRT
<213> *Saccharomyces cerevisiae*

<220>
<223> Figure 8(b)

<400> 22

Met Leu Ser Lys Val Leu Leu Asn Ile Ala Phe Lys Val Leu Leu Thr
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Thr Ala Lys Arg Ala Val Asp Pro Asp Asp Asp Asp Glu Leu Leu Pro
20 25 30

Ser Pro Asp Leu Pro Gly Ser Asp Asp Pro Ile Ala Gly Asp Pro Asp
35 40 45

Val Asp Leu Asn Pro Val Thr Glu Glu Met Phe Ser Ser Trp Ala Leu
50 55 60

Phe Ile Met Leu Leu Leu Leu Ile Ser Ala Leu Trp Ser Ser Tyr Tyr
65 70 75 80

Leu Thr Gln Lys Arg Ile Arg Ala Val His Glu Thr Val Leu Ser Ile
85 90 95

Phe Tyr Gly Met Val Ile Gly Leu Ile Ile Arg Met Ser Pro Gly His
100 105 110

Tyr Ile Gln Asp Thr Val Thr Phe Asn Ser Ser Tyr Phe Phe Asn Val
115 120 125

Leu Leu Pro Pro Ile Ile Leu Asn Ser Gly Tyr Glu Leu Asn Gln Val
130 135 140

Asn Phe Phe Asn Asn Met Leu Ser Ile Leu Ile Phe Ala Ile Pro Gly
145 150 155 160

Thr Phe Ile Ser Ala Val Val Ile Gly Ile Ile Leu Tyr Ile Trp Thr
165 170 175

Phe Leu Gly Leu Glu Ser Ile Asp Ile Ser Phe Ala Asp Ala Met Ser

180										185					190				
Val	Gly	Ala	Thr	Leu	Ser	Ala	Thr	Asp	Pro	Val	Thr	Ile	Leu	Ser	Ile				
		195					200					205							
Phe	Asn	Ala	Tyr	Lys	Val	Asp	Pro	Lys	Leu	Tyr	Thr	Ile	Ile	Phe	Gly				
	210					215					220								
Glu	Ser	Leu	Leu	Asn	Asp	Ala	Ile	Ser	Ile	Val	Met	Phe	Glu	Thr	Cys				
225					230					235					240				
Gln	Lys	Phe	His	Gly	Gln	Pro	Ala	Thr	Phe	Ser	Ser	Val	Phe	Glu	Gly				
				245					250					255					
Ala	Gly	Leu	Phe	Leu	Met	Thr	Phe	Ser	Val	Ser	Leu	Leu	Ile	Gly	Val				
			260					265					270						
Leu	Ile	Gly	Ile	Leu	Val	Ala	Leu	Leu	Leu	Lys	His	Thr	His	Ile	Arg				
	275						280					285							
Arg	Tyr	Pro	Gln	Ile	Glu	Ser	Cys	Leu	Ile	Leu	Leu	Ile	Ala	Tyr	Glu				
	290					295					300								
Ser	Tyr	Phe	Phe	Ser	Asn	Gly	Cys	His	Met	Ser	Gly	Ile	Val	Ser	Leu				
305					310					315					320				
Leu	Phe	Cys	Gly	Ile	Thr	Leu	Lys	His	Tyr	Ala	Tyr	Tyr	Asn	Met	Ser				
				325					330				335						
Arg	Arg	Ser	Gln	Ile	Thr	Ile	Lys	Tyr	Ile	Phe	Gln	Leu	Leu	Ala	Arg				
			340					345					350						
Leu	Ser	Glu	Asn	Phe	Ile	Phe	Ile	Tyr	Leu	Gly	Leu	Glu	Leu	Phe	Thr				
		355					360					365							
Glu	Val	Glu	Leu	Val	Tyr	Lys	Pro	Leu	Leu	Ile	Ile	Val	Ala	Ala	Ile				
	370					375					380								
Ser	Ile	Cys	Val	Ala	Arg	Trp	Cys	Ala	Val	Phe	Pro	Leu	Ser	Gln	Phe				
385					390					395					400				
Val	Asn	Trp	Ile	Tyr	Arg	Val	Lys	Thr	Ile	Arg	Ser	Met	Ser	Gly	Ile				
				405					410					415					
Thr	Gly	Glu	Asn	Ile	Ser	Val	Pro	Asp	Glu	Ile	Pro	Tyr	Asn	Tyr	Gln				
			420					425					430						
Met	Met	Thr	Phe	Trp	Ala	Gly	Leu	Arg	Gly	Ala	Val	Gly	Val	Ala	Leu				
		435					440					445							
Ala	Leu	Gly	Ile	Gln	Gly	Glu	Tyr	Lys	Phe	Thr	Leu	Leu	Ala	Thr	Val				
		450				455					460								
Leu	Val	Val	Val	Val	Leu	Thr	Val	Ile	Ile	Phe	Gly	Gly	Thr	Thr	Ala				
465					470					475					480				
Gly	Met	Leu	Glu	Val	Leu	Asn	Ile	Lys	Thr	Gly	Cys	Ile	Ser	Glu	Glu				

485										490					495				
Asp	Thr	Ser	Asp	Asp	Glu	Phe	Asp	Ile	Glu	Ala	Pro	Arg	Ala	Ile	Asn				
			500					505					510						
Leu	Leu	Asn	Gly	Ser	Ser	Ile	Gln	Thr	Asp	Leu	Gly	Pro	Tyr	Ser	Asp				
		515					520					525							
Asn	Asn	Ser	Pro	Asp	Ile	Ser	Ile	Asp	Gln	Phe	Ala	Val	Ser	Ser	Asn				
		530				535					540								
Lys	Asn	Leu	Pro	Asn	Asn	Ile	Ser	Thr	Thr	Gly	Gly	Asn	Thr	Phe	Gly				
545					550					555					560				
Gly	Leu	Asn	Glu	Thr	Glu	Asn	Thr	Ser	Pro	Asn	Pro	Ala	Arg	Ser	Ser				
				565					570					575					
Met	Asp	Lys	Arg	Asn	Leu	Arg	Asp	Lys	Leu	Gly	Thr	Ile	Phe	Asn	Ser				
			580					585					590						
Asp	Ser	Gln	Trp	Phe	Gln	Asn	Phe	Asp	Glu	Gln	Val	Leu	Lys	Pro	Val				
		595					600					605							
Phe	Leu	Asp	Asn	Val	Ser	Pro	Ser	Leu	Gln	Asp	Ser	Ala	Thr	Gln	Ser				
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Pro	Ala	Asp	Phe	Ser	Ser	Gln	Asn	His											
625					630														

<210> 23
 <211> 378
 <212> DNA
 <213> Oryza sativa

<220>
 <223> Figure 8(c); n=unkown

<400> 23

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cttctgtggt attgtaatgt cacattacac ttggcataac gtcacagaga gttcaagagt 180
tacaacaaag cacgcatttg caactctgtc cttcattgct gagacttttc tcttctgta 240
tgttgggatg gatgcattgg atattgaaaa atgggagntt nccagtgaca gacctggnaa 300
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<210> 24
 <211> 268
 <212> DNA
 <213> Oryza sativa

<220>
 <223> Figure 8 (d); n=unknown

<400> 24

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gcgtctgcat cgctgctggc cacctcctcg aggagagccg atggatgaac gagtccatca 180
ccgcgctaata catcggggtt ggtacttgga ggagtgnntt tgnatgggtg cgagctggaa 240
gcactcgna tactgggtgt cagcgagg 268
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<210> 25 <211> 380

<212> DNA

<213> *Oryza sativa*

<220>

<223> Figure 8(e); n=unknown

<400> 25

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attgtctggc atcaaaactat gccagccac tgatggcacg gctcagttta atgaggctgg 180
ccacaccttc tccagtggga gttatctgtg catctaattg gtaccttctt tgtattgtag 240
ttgttacttt acccttgatt tggtcgggtt gcttctaaag caggttgtga aattcctatt 300
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ctattaaaaa aaaaaaaaaa 380
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<210> 26

<211> 596

<212> DNA

<213> *Medicago truncatula*

<220>

<223> Figure 8(f); n=unknown

<400> 26

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aattttattc ttcatatata tatatatata tatccaatta accatctcaa tctcatattc 180
acatatacct cataaaccat ccataacatc cttaaaaacc ctctaagccc tttcaaactt 240
tgatttgtaa ttgtttctct tataagtctt aacctgcaca aatcaatttt aatttcttat 300
gttcatatag ttatgaatga ttgaaaaaaa cacaaatgac tccagttatc tgtgagatct 360
ctatgataaa ctctactctc cagacgcagg acacatttag ttcaatcttt ctctgttggt 420
ttcctctact gggtctatat tttctcatga attattaatt aatcctatat tctttctttt 480
caatacaaat ttagtttcat taattctatc aacataatca attaaactac atagttagaa 540
aaatagtact attaccacga tcaactcaaag ttttttagtt ttttaacaaac antctg 596
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<210> 27

<211> 522

<212> DNA

<213> *Hordeum vulgare*

<220>

<223> Figure 8(g); n=unknown

<400> 27

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gcatgatga aacttgatga tcagtttttt tagttgaaaa attctgcaag aacagctact 180
taatgctcta ttgtgtatcg caggcacaca tcagctgctg atgtctgcta tacttctgta 240
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gctagtatgt atactctcac atcatatgct actgttctat atagaactat gtgatagcta 360
ctgctatact gctgtcatat agagtcctcg taatatcaat gctattttgc tttcctcaaa 420
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<210> 28
 <211> 330
 <212> DNA
 <213> *Arabidopsis thaliana*

<220>
 <223> Figure 8(h); n=unknown <400> 28

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gcatacaaca agtttacaag ggccgggcac acagatgtac gngggaatgc aatcatgac 180
acngtacgn taactgtctg tntttttagc acagtgggtg ttggatgct gaccaaacca 240
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attncaaata acccnaanaa tcnatacca 330

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<210> 29
 <211> 633
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<220>
 <223> Figure 2(a)

<400> 29

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Thr	Ala	Lys	Arg	Ala	Val	Asp	Pro	Asp	Asp	Asp	Asp	Glu	Leu	Leu	Pro
			20					25					30		
Ser	Pro	Asp	Leu	Pro	Gly	Ser	Asp	Asp	Pro	Ile	Ala	Gly	Asp	Pro	Asp
		35					40					45			
Val	Asp	Leu	Asn	Pro	Val	Thr	Glu	Glu	Met	Phe	Ser	Ser	Trp	Ala	Leu
	50					55					60				
Phe	Ile	Met	Leu	Leu	Leu	Leu	Ile	Ser	Ala	Leu	Trp	Ser	Ser	Tyr	Tyr
65					70				75					80	
Leu	Thr	Gln	Lys	Arg	Ile	Arg	Ala	Val	His	Glu	Thr	Val	Leu	Ser	Ile
				85				90						95	
Phe	Tyr	Gly	Met	Val	Ile	Gly	Leu	Ile	Ile	Arg	Met	Ser	Pro	Gly	His

100										105					110						
Tyr	Ile	Gln	Asp	Thr	Val	Thr	Phe	Asn	Ser	Ser	Tyr	Phe	Phe	Asn	Val						
		115						120					125								
Leu	Leu	Pro	Pro	Ile	Ile	Leu	Asn	Ser	Gly	Tyr	Glu	Leu	Asn	Gln	Val						
		130					135					140									
Asn	Phe	Phe	Asn	Asn	Met	Leu	Ser	Ile	Leu	Ile	Phe	Ala	Ile	Pro	Gly						
145					150					155					160						
Thr	Phe	Ile	Ser	Ala	Val	Val	Ile	Gly	Ile	Ile	Leu	Tyr	Ile	Trp	Thr						
				165					170					175							
Phe	Leu	Gly	Leu	Glu	Ser	Ile	Asp	Ile	Ser	Phe	Ala	Asp	Ala	Met	Ser						
			180					185					190								
Val	Gly	Ala	Thr	Leu	Ser	Ala	Thr	Asp	Pro	Val	Thr	Ile	Leu	Ser	Ile						
		195						200					205								
Phe	Asn	Ala	Tyr	Lys	Val	Asp	Pro	Lys	Leu	Tyr	Thr	Ile	Ile	Phe	Gly						
		210				215					220										
Glu	Ser	Leu	Leu	Asn	Asp	Ala	Ile	Ser	Ile	Val	Met	Phe	Glu	Thr	Cys						
225					230					235					240						
Gln	Lys	Phe	His	Gly	Gln	Pro	Ala	Thr	Phe	Ser	Ser	Val	Phe	Glu	Gly						
				245					250					255							
Ala	Gly	Leu	Phe	Leu	Met	Thr	Phe	Ser	Val	Ser	Leu	Leu	Ile	Gly	Val						
			260					265					270								
Leu	Ile	Gly	Ile	Leu	Val	Ala	Leu	Leu	Leu	Lys	His	Thr	His	Ile	Arg						
		275					280						285								
Arg	Tyr	Pro	Gln	Ile	Glu	Ser	Cys	Leu	Ile	Leu	Leu	Ile	Ala	Tyr	Glu						
		290				295					300										
Ser	Tyr	Phe	Phe	Ser	Asn	Gly	Cys	His	Met	Ser	Gly	Ile	Val	Ser	Leu						
305					310					315					320						
Leu	Phe	Cys	Gly	Ile	Thr	Leu	Lys	His	Tyr	Ala	Tyr	Tyr	Asn	Met	Ser						
				325					330					335							
Arg	Arg	Ser	Gln	Ile	Thr	Ile	Lys	Tyr	Ile	Phe	Gln	Leu	Leu	Ala	Arg						
			340					345					350								
Leu	Ser	Glu	Asn	Phe	Ile	Phe	Ile	Tyr	Leu	Gly	Leu	Glu	Leu	Phe	Thr						
		355					360					365									
Glu	Val	Glu	Leu	Val	Tyr	Lys	Pro	Leu	Leu	Ile	Ile	Val	Ala	Ala	Ile						
		370				375					380										
Ser	Ile	Cys	Val	Ala	Arg	Trp	Cys	Ala	Val	Phe	Pro	Leu	Ser	Gln	Phe						
385					390					395					400						
Val	Asn	Trp	Ile	Tyr	Arg	Val	Lys	Thr	Ile	Arg	Ser	Met	Ser	Gly	Ile						

405										410					415				
Thr	Gly	Glu	Asn	Ile	Ser	Val	Pro	Asp	Glu	Ile	Pro	Tyr	Asn	Tyr	Gln				
420										425					430				
Met	Met	Thr	Phe	Trp	Ala	Gly	Leu	Arg	Gly	Ala	Val	Gly	Val	Ala	Leu				
435										440					445				
Ala	Leu	Gly	Ile	Gln	Gly	Glu	Tyr	Lys	Phe	Thr	Leu	Leu	Ala	Thr	Val				
450										455					460				
Leu	Val	Val	Val	Val	Leu	Thr	Val	Ile	Ile	Phe	Gly	Gly	Thr	Thr	Ala				
465										470					475				
Gly	Met	Leu	Glu	Val	Leu	Asn	Ile	Lys	Thr	Gly	Cys	Ile	Ser	Glu	Glu				
485										490					495				
Asp	Thr	Ser	Asp	Asp	Glu	Phe	Asp	Ile	Glu	Ala	Pro	Arg	Ala	Ile	Asn				
500										505					510				
Leu	Leu	Asn	Gly	Ser	Ser	Ile	Gln	Thr	Asp	Leu	Gly	Pro	Tyr	Ser	Asp				
515										520					525				
Asn	Asn	Ser	Pro	Asp	Ile	Ser	Ile	Asp	Gln	Phe	Ala	Val	Ser	Ser	Asn				
530										535					540				
Lys	Asn	Leu	Pro	Asn	Asn	Ile	Ser	Thr	Thr	Gly	Gly	Asn	Thr	Phe	Gly				
545										550					555				
Gly	Leu	Asn	Glu	Thr	Glu	Asn	Thr	Ser	Pro	Asn	Pro	Ala	Arg	Ser	Ser				
565										570					575				
Met	Asp	Lys	Arg	Asn	Leu	Arg	Asp	Lys	Leu	Gly	Thr	Ile	Phe	Asn	Ser				
580										585					590				
Asp	Ser	Gln	Trp	Phe	Gln	Asn	Phe	Asp	Glu	Gln	Val	Leu	Lys	Pro	Val				
595										600					605				
Phe	Leu	Asp	Asn	Val	Ser	Pro	Ser	Leu	Gln	Asp	Ser	Ala	Thr	Gln	Ser				
610										615					620				
Pro	Ala	Asp	Phe	Ser	Ser	Gln	Asn	His											
625										630									

<210> 30

<211> 669

<212> PRT

<213> Homo sapiens

<220>

<223> Figure 2(a) HsNHE6 Na⁺/H⁺ exchanger (GenBank
Accession No. 2944237)

<400> 30

Met Ala Arg Arg Gly Trp Arg Arg Ala Pro Leu Arg Arg Gly Val Gly

1	5	10	15
Ser Ser Pro Arg Ala Arg Arg Leu Met Arg Pro Leu Trp Leu Leu Leu	20	25	30
Ala Val Gly Val Phe Asp Trp Ala Gly Ala Ser Asp Gly Gly Gly Gly	35	40	45
Glu Ala Arg Ala Met Asp Glu Glu Ile Val Ser Glu Lys Gln Ala Glu	50	55	60
Glu Ser His Arg Gln Asp Ser Ala Asn Leu Leu Ile Phe Ile Leu Leu	65	70	75
Leu Thr Leu Thr Ile Leu Thr Ile Trp Leu Phe Lys His Arg Arg Ala	85	90	95
Arg Phe Leu His Glu Thr Gly Leu Ala Met Ile Tyr Gly Leu Leu Val	100	105	110
Gly Leu Val Leu Arg Tyr Gly Ile His Val Pro Ser Asp Val Asn Asn	115	120	125
Val Thr Leu Ser Cys Glu Val Gln Ser Ser Pro Thr Thr Leu Leu Val	130	135	140
Thr Phe Asp Pro Glu Val Phe Phe Asn Ile Leu Leu Pro Pro Ile Ile	145	150	155
Phe Tyr Ala Gly Tyr Ser Leu Lys Arg Arg His Phe Phe Arg Asn Leu	165	170	175
Gly Ser Ile Leu Ala Tyr Ala Phe Leu Gly Thr Ala Ile Ser Cys Phe	180	185	190
Val Ile Gly Ser Ile Met Tyr Gly Cys Val Thr Leu Met Lys Val Thr	195	200	205
Gly Gln Leu Ala Gly Asp Phe Tyr Phe Thr Asp Cys Leu Leu Phe Gly	210	215	220
Ala Ile Val Ser Ala Thr Asp Pro Val Thr Val Leu Ala Ile Phe His	225	230	235
Glu Leu Gln Val Asp Val Glu Leu Tyr Ala Leu Leu Phe Gly Glu Ser	245	250	255
Val Leu Asn Asp Ala Val Ala Ile Val Leu Ser Ser Ser Ile Val Ala	260	265	270
Tyr Gln Pro Ala Gly Asp Asn Ser His Thr Phe Asp Val Thr Ala Met	275	280	285
Phe Lys Ser Ile Gly Ile Phe Leu Gly Ile Phe Ser Gly Ser Phe Ala	290	295	300
Met Gly Ala Ala Thr Gly Val Val Thr Ala Leu Val Thr Lys Phe Thr			

305					310					315				320	
Lys	Leu	Arg	Glu	Phe	Gln	Leu	Leu	Glu	Thr	Gly	Leu	Phe	Phe	Leu	Met
				325					330					335	
Ser	Trp	Ser	Thr	Phe	Leu	Leu	Ala	Glu	Ala	Trp	Gly	Phe	Thr	Gly	Val
			340					345					350		
Val	Ala	Val	Leu	Phe	Cys	Gly	Ile	Thr	Gln	Ala	His	Tyr	Thr	Tyr	Asn
		355					360					365			
Asn	Leu	Ser	Thr	Glu	Ser	Gln	His	Arg	Thr	Lys	Gln	Leu	Phe	Glu	Leu
	370					375					380				
Leu	Asn	Phe	Leu	Ala	Glu	Asn	Phe	Ile	Phe	Ser	Tyr	Met	Gly	Leu	Thr
385					390					395					400
Leu	Phe	Thr	Phe	Gln	Asn	His	Val	Phe	Asn	Pro	Thr	Phe	Val	Val	Gly
				405					410						415
Ala	Phe	Val	Ala	Ile	Phe	Leu	Gly	Arg	Ala	Ala	Asn	Ile	Tyr	Pro	Leu
			420					425					430		
Ser	Leu	Leu	Leu	Asn	Leu	Gly	Arg	Arg	Ser	Lys	Ile	Gly	Ser	Asn	Phe
		435					440					445			
Gln	His	Met	Met	Met	Phe	Ala	Gly	Leu	Arg	Gly	Ala	Met	Ala	Phe	Ala
	450					455					460				
Leu	Ala	Ile	Arg	Asp	Thr	Ala	Thr	Tyr	Ala	Arg	Gln	Met	Met	Phe	Ser
465					470					475					480
Thr	Thr	Leu	Leu	Ile	Val	Phe	Phe	Thr	Val	Trp	Val	Phe	Gly	Gly	Gly
				485					490					495	
Thr	Thr	Ala	Met	Leu	Ser	Cys	Leu	His	Ile	Arg	Val	Gly	Val	Asp	Ser
			500					505					510		
Asp	Gln	Glu	His	Leu	Gly	Val	Pro	Glu	Asn	Glu	Arg	Arg	Thr	Thr	Lys
		515					520					525			
Ala	Glu	Ser	Ala	Trp	Leu	Phe	Arg	Met	Trp	Tyr	Asn	Phe	Asp	His	Asn
	530					535					540				
Tyr	Leu	Lys	Pro	Leu	Leu	Thr	His	Ser	Gly	Pro	Pro	Leu	Thr	Thr	Thr
545					550					555					560
Leu	Pro	Ala	Cys	Cys	Gly	Pro	Ile	Ala	Arg	Cys	Leu	Thr	Ser	Pro	Gln
				565					570					575	
Ala	Tyr	Glu	Asn	Gln	Glu	Gln	Leu	Lys	Asp	Asp	Asp	Ser	Asp	Leu	Ile
			580					585					590		
Leu	Asn	Asp	Gly	Asp	Ile	Ser	Leu	Thr	Tyr	Gly	Asp	Ser	Thr	Val	Asn
		595					600					605			
Thr	Glu	Pro	Ala	Thr	Ser	Ser	Ala	Pro	Arg	Arg	Phe	Met	Gly	Asn	Ser

610	615	620
Ser Glu Asp Ala Leu Asp Arg Glu Leu Ala Phe Gly Asp His Glu Leu		
625	630	635 640
Val Ile Arg Gly Thr Arg Leu Val Leu Pro Met Asp Asp Ser Glu Pro		
	645	650 655
Pro Leu Asn Leu Leu Asp Asn Thr Arg His Gly Pro Ala		
	660	665

<210> 31
 <211> 541
 <212> PRT
 <213> C. elegans

<220>
 <223> Figure 2(a) CeNHE1 (GenBank Accession No. 3877723)

<400> 31

Met Lys Val Glu Ser Leu Phe Phe Met Ser Gln Thr Phe Asp Val Ile		
1	5	10 15
Thr Lys Asn Lys Thr Ile Val Lys Glu Pro Pro Asp Tyr Leu Met Leu		
	20	25 30
Glu Val Lys Pro Glu Gly Gly Ser Arg Val Ser Phe His Tyr Glu Leu		
	35	40 45
Ile Glu Gly Phe Phe Ala Asp Lys Arg Lys Lys Ile Glu Gln Gln Ile		
	50	55 60
Glu Gln Lys Ser Val Phe Ser Pro Glu Val Phe Phe Asn Met Leu Ile		
	65	70 75 80
Pro Pro Ile Ile Phe Asn Ala Gly Tyr Ser Leu Lys Lys Arg His Phe		
	85	90 95
Phe Arg Asn Ile Gly Ser Ile Leu Ala Ile Val Phe Ile Gly Thr Thr		
	100	105 110
Ile Ser Cys Phe Gly Thr Gly Cys Leu Met Phe Val Phe Thr Ser Ile		
	115	120 125
Phe Gln Met Gly Tyr Ser Phe Lys Glu Leu Leu Phe Phe Gly Ala Leu		
	130	135 140
Ile Ser Ala Thr Asp Pro Val Thr Ile Ile Ser Val Phe Asn Asp Met		
	145	150 155 160
Asn Val Glu Ala Asp Leu Phe Ala Leu Ile Phe Gly Glu Ser Ala Leu		
	165	170 175
Asn Asp Ala Val Ala Ile Val Leu Ser Glu Val Ile Glu Asn Phe Ser		
	180	185 190

Thr Ser Ser Glu Ala Ile Thr Leu Gln Asp Phe Gly Ser Ala Ile Ala
 195 200 205
 Gly Phe Ala Gly Val Phe Phe Gly Ser Leu Met Leu Gly Phe Met Ile
 210 215 220
 Gly Cys Met Asn Ala Phe Leu Thr Lys Met Thr Leu Ile Ser Glu His
 225 230 235 240
 Ala Leu Leu Glu Ser Ser Leu Phe Val Leu Ile Ser Tyr Ile Ser Phe
 245 250 255
 Leu Val Ala Glu Val Cys Gly Leu Thr Gly Ile Val Ser Val Leu Phe
 260 265 270
 Cys Gly Ile Ala Gln Ala His Tyr Thr Tyr Asn Asn Leu Ser Asp Glu
 275 280 285
 Ser Gln Ser Asn Thr Lys His Phe Phe His Met Val Ser Phe Ile Met
 290 295 300
 Glu Ser Phe Ile Phe Cys Tyr Ile Gly Val Ser Val Phe Val Thr Asn
 305 310 315 320
 Asn Gln Arg Trp Ser Phe Ser Phe Leu Leu Phe Ser Leu Ile Ser Ile
 325 330 335
 Thr Ala Ser Arg Ala Leu Phe Val Tyr Pro Leu Ser Trp Leu Leu Asn
 340 345 350
 Ile Arg Arg Arg Pro Lys Ile Pro Lys Arg Tyr Gln His Met Ile Leu
 355 360 365
 Phe Ala Gly Leu Arg Gly Ala Met Ala Phe Ala Leu Ala Gly Arg Asn
 370 375 380
 Thr Ser Thr Glu Asn Arg Gln Met Ile Phe Ala Thr Thr Thr Ala Val
 385 390 395 400
 Val Ile Val Thr Val Leu Val Asn Gly Gly Leu Thr Ser Trp Met Ile
 405 410 415
 Asp Tyr Leu Gln Ile Lys His Gly Lys Asp Ala Ile Glu Glu Gly Gln
 420 425 430
 Arg Leu Glu Asn Ser Met Ser Ser Ser Pro Ala Asp Gln His Ser Asp
 435 440 445
 Leu Asp Glu Ser Val Pro Val Thr Met Ser Pro Gly Leu Asn Pro Trp
 450 455 460
 Asp Lys Ala Phe Leu Pro Arg Lys Trp Tyr His Phe Asp Ala Arg Trp
 465 470 475 480
 Gln Leu Leu Lys Leu Val Phe Gln Phe His Glu Thr Ser Thr Asp Pro
 485 490 495

Cys Asp Ala Ile Phe Gly Thr Asn Thr Pro Thr Val Leu Ser Ser Ile
500 505 510

Asp Phe Leu Val Asp Phe Lys Pro Ser Thr Arg Val Arg Gln Cys Arg
515 520 525

Ala Leu Gln Tyr Asn Cys Thr Ile Arg Asp Ser Ile Asp
530 535 540

<210> 32
<211> 21
<212> DNA
<213> Synthetic

<220>
<223> Page 54 - PCR forward primer (X6F)

<400> 32

cctcaggtga taccaatctc a

21

<210> 33
<211> 20
<212> DNA
<213> Synthetic

<220>
<223> Page 54 - PCR reverse primer (X6REV)

<400> 33

gatccaatgt aacaccggag

20

<210> 34
<211> 19
<212> DNA
<213> Synthetic

<220>
<223> Page 54 - PCR forward primer (NHX7F)

<400> 34

ttcgttctcg gccatgtcc

19

<210> 35
<211> 22
<212> DNA
<213> Synthetic

<220>
<223> Page 54 - PCR reverse primer (NHX7REV)

<400> 35

cggagagacc aacaccttct gc

22

<210> 36

<211> 24

<212> DNA

<213> Synthetic

<220>

<223> Page 37 - preferred oligonucleotide probe

<400> 36

ttcttcatat atcttttgcc accc

24

<210> 37

<211> 30

<212> DNA

<213> Synthetic

<220>

<223> Page 55 - Primer

<400> 37

cgcgtcgaca tggtggattc tctagtgtcg

30